Coding Challenge 4

Prativa Chhetri and Karamjit Kaur Baryah

2025-02-27

Table of Contents

# Link for the Paper

* [Link for paper](https://doi.org/10.1094/PDIS-06-21-1253-RE)

# Q1

*In the context of R Markdown , the YAML header appears at the top of the document, enclosed by — lines, and it contains metadata about the document.* *Literate Programming(For eg. R Markdown) is documentation and code live together in the same file, making it easy for others (and your future self!) to understand not just what the code does, but why it was written that way.*

# Q2

## 2 (B)

mycotoxin=read.csv("MycotoxinData.csv", na.strings = "na")  
mycotoxin$Treatment <- as.factor(mycotoxin$Treatment)  
mycotoxin$Cultivar <- as.factor(mycotoxin$Cultivar)

## 2(C)

### CbbPalette

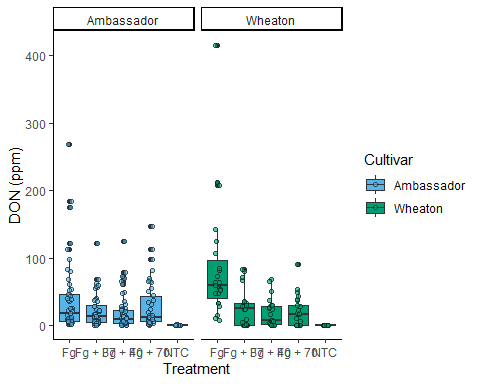
cbbPalette <- c("#56B4E9", "#009E73")

### DON\_PLOT1

Plot1 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot() + # add boxplot layer  
 xlab("Treatment") +   
 ylab("DON (ppm)") + # y label  
 geom\_point(alpha = 0.6,pch = 21, color = "black", position = position\_jitterdodge()) +  
 scale\_fill\_manual(values = cbbPalette)+ # transparency of the jittered points to 0.6. #Jitter points over the boxplot and fill the points and boxplots Cultivar with two colors from the cbbPallete   
 facet\_wrap(~Cultivar)+ #faceted by Cultivar  
 theme\_classic() # for classic theme   
Plot1

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

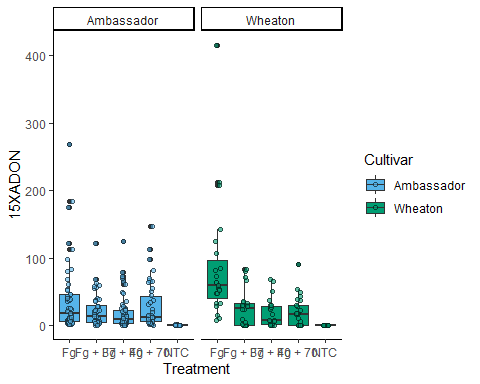


### 15XADON\_PLOT2

Plot2 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot() + # add boxplot layer  
 xlab("Treatment") +   
 ylab("15XADON") + # y label  
 geom\_point(alpha = 0.6,pch = 21, color = "black", position = position\_jitterdodge()) +  
 scale\_fill\_manual(values = cbbPalette)+ # transparency of the jittered points to 0.6. #Jitter points over the boxplot and fill the points and boxplots Cultivar with two colors from the cbbPallete   
 facet\_wrap(~Cultivar)+ #faceted by Cultivar  
 theme\_classic() # for classic theme   
  
Plot2

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

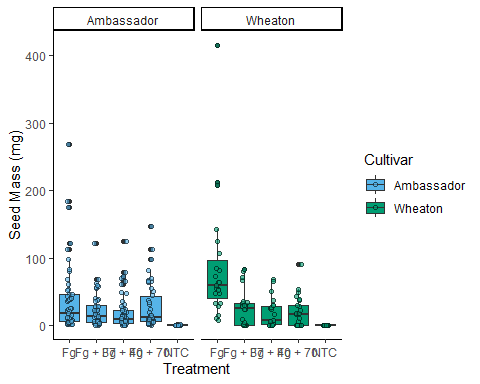


### SeedMass\_PLOT3

Plot3 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot() + # add boxplot layer  
 xlab("Treatment") +   
 ylab("Seed Mass (mg)") + # y label  
 geom\_point(alpha = 0.6,pch = 21, color = "black", position = position\_jitterdodge()) +  
 scale\_fill\_manual(values = cbbPalette)+ # transparency of the jittered points to 0.6. #Jitter points over the boxplot and fill the points and boxplots Cultivar with two colors from the cbbPallete   
 facet\_wrap(~Cultivar)+ #faceted by Cultivar  
 theme\_classic() # for classic theme   
Plot3

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).



### 3Combined\_PLOT

figure=ggarrange(  
 Plot1,  
 Plot2,  
 Plot3,  
 labels = c("A", "B", "C"),  
 nrow = 1,  
 ncol = 3,  
 common.legend=TRUE  
)

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

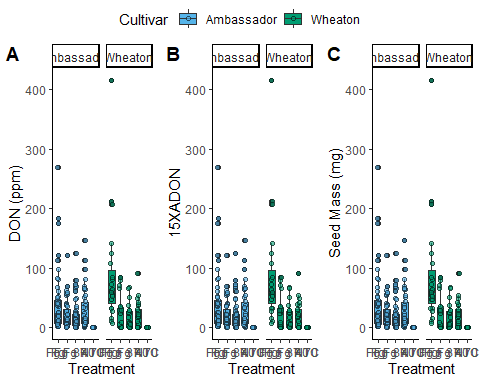
## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

figure



# Q(5)

*ALso available in GitHub Mycotoxin Repository*

* [README](README.md)

# Q(6)

*Link TO GitHub respository along with README*

* [GitHub Link](https://github.com/PrativaC/Mycotoxin)